

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 6, 2002, 13:35:49 ; Search time 19.47 seconds
(without alignments)
2527.415 Million cell updates/sec

Title: US-09-405-504A-25
Perfect score: 3372
Sequence: 1 MRAPGAGAAVSVSLALLWLL.....HYLPLNEAVVTRICSGAFAL 646

Scoring table: BLOSUM62
Gap 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues
Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	3054	90.6	646	1 A55093	fatty acid transp
2	1267.5	37.6	650	2 T21498	hypothetical prote
3	1257.5	37.3	655	2 T15879	hypothetical prote
4	988.5	29.3	689	1 JW0107	very-long-chain ac
5	899.5	26.7	597	2 D70609	probable fadD6 pro
6	872	25.9	608	2 H83284	probable very-long
7	747.5	22.2	643	2 T43052	fatty acid transp
8	699	20.7	623	2 S45899	probable membrane
9	406.5	12.1	522	2 H85484	probable crotonob
10	390.5	11.6	522	2 S40558	probable carnitine
11	377	11.2	502	2 D70806	probable fadD17 pr
12	372	11.0	532	2 G70986	probable coA ligas
13	361	10.7	2723	2 T03221	probable polyketid
14	346.5	10.3	503	2 E70853	probable acid--CoA
15	325	9.6	444	2 T50931	hypothetical prote
16	323.5	9.6	549	2 E69893	probable acid--CoA
17	320	9.5	593	2 E69378	probable acid--CoA
18	319	9.5	549	2 T44812	probable acid--CoA
19	316	9.4	513	2 A49831	probable fatty-aci
20	315	9.3	999	2 B70501	probable acid--CoA
21	307	9.1	486	2 H69656	hypothetical prote
22	305	9.0	560	2 A70628	O-succinylbenzoate
23	301.5	8.9	2560	1 T40457	probable acid--CoA
24	300.5	8.9	599	2 H72454	peptide synthetase
25	299	8.9	3588	2 T40485	probable fatty-aci
26	298.5	8.9	544	1 S01667	surfactin syntheta
27	297.5	8.8	544	2 S15695	4-coumarate--CoA 1
28	294	8.7	514	2 T46131	4-coumarate--CoA 1
29	291.5	8.6	8563	2 T30226	polyketide synthas

30	289.5	8.6	557	2	T07909	4-coumarate--CoA 1
31	289.5	8.6	4735	2	T17463	rifamycin polyketi
32	288.5	8.6	569	2	C69471	probable fatty-aci
33	287.5	8.5	3587	2	T40486	surfactin syntheta
34	286.5	8.5	535	2	T08074	4-coumarate--CoA 1
35	286.5	8.5	552	2	E69438	probable fatty-aci
36	286.5	8.5	566	2	D85778	probable ligase/sy
37	284.5	8.4	493	2	G84263	long-chain fatty-a
38	282.5	8.4	548	2	T07908	4-coumarate--CoA 1
39	281.5	8.3	546	2	C83791	acid-CoA ligase BH
40	281.5	8.3	561	2	D96674	hypothetical prote
41	281	8.3	563	1	JU0311	4-coumarate--CoA 1
42	280.5	8.3	566	2	E64928	probable acid--CoA
43	278.5	8.3	545	1	B39827	4-coumarate--CoA 1
44	277.5	8.2	545	1	A39827	4-coumarate--CoA 1
45	277	8.2	551	2	H69371	probable acid--CoA

ALIGNMENTS

RESULT 1

A55093

fatty acid transport protein precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 08-Sep-2000

C:Accession: A55093; I49132

R:Schaffer, J.E.; Lodish, H.F.

Cell 79, 427-436, 1994

A:Title: Expression cloning and characterization of a novel adipocyte long chain

A:Reference number: A55093; MUID:95042740

A:Accession: A55093

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-646 <SCH>

A:Cross-references: GB:U15976; NID:g563828; PIDN:AAC71060.1; PID:g563829

C:Genetics:

A:Gene: FATP

C:Superfamily: Mycobacterium tuberculosis probable fadD6 protein; acetate--CoA lig
F:124-604/Domain: acetate--CoA ligase homology <ACU>

Query Match 90.6%; Score 3054; DB 1; Length 646;

Best Local Similarity 89.5%; Pred. No. 1.9e-237;

Matches 578; Conservative 30; Mismatches 38; Indels 0; Gaps 0;

QY 1 MRAPGAGAAVSVSLALLWLLGLPWTWSAAAALGVYVGGGWRFLRVCKTARRDLFGLSV 60

Db 1 MRAPGAGTASVASLALLWLLGLPWTWSAAAALGVYVGGGWRFLRVCKTARRDLFGLSV 60

QY 61 LIRVRLRHRHAGHTIPRIFQAVVORQPERIALVDAGTGCWTFQAQLDAYSNVANLF 120

Db 61 LIRVRLRHRHAGHTIPRIFQAVVORQPERIALVDAGTGCWTFQAQLDAYSNVANLF 120

QY 121 RQLGFAPGDVVAFLEGRPEFVGLWLGLAKAGMEALLNVRERPLAFLCLTSGAKALI 180

Db 121 RQLGFAPGDVVAFLEGRPEFVGLWLGLAKAGMEALLNVRERPLAFLCLTSGAKALI 180

QY 181 FGGEMAAVAEVSGLKSLKFCSDGLGPESILPTDTHLLDPLLEKASTAPLAQIPSKGM 240

Db 181 YGGEMAAVAEVSGLKSLKFCSDGLGPESILPTDTHLLDPLLEKASTAPLAQIPSKGM 240

QY 241 DDLRFYIYTSGLTGLPKAAIVHSRYRMAAFHGHYRMAQADVLDYCLPLVHSAAGNIIG 300

Db 241 DDLRFYIYTSGLTGLPKAAIVHSRYRMAAFHGHYRMAQADVLDYCLPLVHSAAGNIIG 300

QY 301 VGCLYIGTVLVRKKFSASRFWDDCIKYNTQVQVIGETICRYLLKQPYREARRHRVRL 360

Db 301 VGCLYIGTVLVRKKFSASRFWDDCIKYNTQVQVIGETICRYLLKQPYREARRHRVRL 360

QY 361 AVNGLRPAIWEETFERFGRVQIGEFYATECNCSIANMDGVGSGGFSNRILPHYVPIR 420

Db 361 AVNGLRPAIWEETFERFGRVQIGEFYATECNCSIANMDGVGSGGFSNRILPHYVPIR 420

Db 542 RVRSINCHRRRRVDIRFALAKHARDRLPGVAVPLFLRVTFPALEYTGTLKIQKGLKQ 601
QY 607 EGPDPRTS--DRLFFDLKOGHYPLNE 633
Db 602 EGIDPDKISGEDKLYLWLPGPSDIYLPFGK 630

RESULT 8

S45899
probable membrane protein YBR041w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YBR0411
C;Species: Saccharomyces cerevisiae
C;Date: 26-Aug-1994 #sequence_revision 09-Sep-1994 #text_change 02-Sep-2000
C;Accession: S45899
R;Andre, B.; Cziepluch, C.; Hein, C.; Jauniaux, J.C.; Urrestarazu, A.; Visser, S.
submitted to the Protein Sequence Database, August 1994

A;Reference number: S45899
A;Accession: S45899
A;Molecule type: DNA
A;Residues: 1-623 <AND>
A;Cross-references: EMBL:235910; NID:g536263; PIDN:CAA84983.1; PID:g536264; MIPS:YBR041w
A;Experimental source: strain S288C

C;Genetics:
A;Gene: SGD:FAT1
A;Cross-references: SGD:S0000245; MIPS:YBR041w
A;Map position: 2R
C;Superfamily: Mycobacterium tuberculosis probable fadD6 protein; acetate--CoA ligase h
C;Keywords: transmembrane protein
F;1-27/Domain: transmembrane #status predicted <TM1>
F;55-71/Domain: transmembrane #status predicted <TM2>
F;133-623/Domain: acetate--CoA ligase homology <ACL>
F;149-167/Domain: transmembrane #status predicted <TM3>
F;304-322/Domain: transmembrane #status predicted <TM4>

Query Match 20.7%; Score 699; DB 2; Length 623;

Best Local Similarity 33.5%; Pred. No. 4.4e-48;
Matches 190; Conservative 87; Mismatches 234; Indels 56; Gaps 19;

QY 66 LEURHORAGHTIPRFQAVVOPELA-----LVDAAGTGCWTFQAOLDAYSNAVAML 119
Db 69 IDVRHRFQNW---YLFQVQONGDHLAISVTRPMAERGEFOLETFYIETV-NIVLR 124
QY 120 FROLGF----APGDVVAIFLEGRPEFVGLWGLAKAGMEAAALLNLRREPLAFCLGTSG 175
Db 125 SHLLHFDYVQAGDYVAIDCTNKLPLVFLWLSLWNGAIPALNTKGTPLVHSLKISN 184
QY 176 AKALIFGGEVAAVAVSVSHLKLKFCSGDLGPE---GILPDTHLLDPLKKEASTAPL 232
Db 185 ITQVFDIPDASNPIRESEEEIKNAL-----PDVKLNYLEEQDLMHELLNSQSPFL 235
QY 233 AQIPSK---GMD--RLFIYITSGTGLPKAAIVVHSRYRMAAFG---HHAYRMAAD 283
Db 236 QQDNVTRPLGLTDFKPSMLIYTSGLTPKSAIM---SWRKSSVCCQVFGVHLMTNES 291
QY 284 VLYDCLPLVHSAAGNIGVQCCLYGLTVVLRKKFSASRPWDCIKYNTVQVYIGEIRY 343
Db 292 TVFTAMPPLFHSAAALIGACAILSHGCLALSHKFSASTFWKQVLTGATHIYVGEVRY 351
QY 344 LLKQPVREARRHRVAVNGLRPAINEEFTEREGRVQIGFEYGATE---CNCSIANMD 400
Db 352 LLHTPLSKYEKMKVAVNGLRPDIDWDFRKNIEVIGFEYAAATPAFTTTFKGD 411
QY 401 GKVGSGFNRSLPHVPIR--LVKV--NEDTMELLRDAOGLICPCQAGEPG-LLAVGIN 455
Db 412 FGIGACRNYGTIIQWFLSQQLVRMDPNDSDV-IYRNSKGECEVAPVGEFGEMLMRIF 470
QY 456 QODPLRDFGCVYES-ATSKKTAHSVFGSGSAYLSGDVLYMDELGYMYFRDRSGDTPRW 514
Db 471 PKKPETSFGYLGNAKETKSVVRDVRFRGDAWYRCGLLKADEYGLWYFLDRMGDTPRW 530
QY 515 RGENSVTTEVEGL--SRLLGQTDVAVYGVAVPGVEGRAGNAVADPHSLLDPA-----I 568

Db 531 KSENVSTTEVEQLTASNKEQYQAVLVVGKVPKEGRAGFAVIKLTDNSLDTITAKTKLL 590
QY 569 YOELOKVLAP-YARPIELRLLPQVDTT 594
Db 591 NDLSLKLNLPSYAMPLVVKFVDEIKMT 617

RESULT 9

H85484
probable crotonobetaine/carnitine-CoA ligase caic [imported] - Escherichia coli (s
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
C;Accession: H85484
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.;
Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; A
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: H85484
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-522 <STO>
A;Cross-references: GB:AE005174; NID:gl2512724; PIDN:AAG54340.1; GSPDB:GN00145; UW
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: caic
C;Superfamily: 4-coumarate--CoA ligase; acetate--CoA ligase homology

Query Match 12.1%; Score 406.5; DB 2; Length 522;
Best Local Similarity 25.9%; Pred. No. 1.1e-24;
Matches 139; Conservative 85; Mismatches 249; Indels 63; Gaps 16;

QY 92 RLALV---DAGTGCWTFQAOLDAYSNAVANLFRQLGAPGDVVAIFLEGRPEFVGLWGL 148
Db 28 KTAICESGGVNVRYSVLEINQEIINTANFLYTLGTRKGDVLAHLNDCPEFIFCMFGL 87
QY 149 AKAGMEAAALLNVRREPLAFCLGTSGAKALIFGGEVAAVAVSVSHLKLKFCSGDL 208
Db 88 AKIGALVMPINARLLREESAWILQNSOACLIVTSAQFVPMYQQIQEQEDATQLRHICLTDV 147
QY 209 ---GPEGLPDTLLDPLKKEASTAPLAQIPSKGMDRLFIYITSGTGLPKAAIVVHSR 265
Db 148 ALPADDGVSSFTQ-----LNQQPATLCYAPPLSTDDELTAEILFTSGTTSRPGVVIH-- 200
QY 266 YRMAAFGHHA---YRMAADVLDCLPLVHSAAGNIIQVGCCLYGLTVVLRKKFSARF 322
Db 201 -YNLRFAGYYSAWQALRDDDDVLTVPAPFHIDCQCTAAMAFSAGATFVLVEKYSARAF 259
QY 323 WDDCIKYNCTVQVYIGEIRYLLKQPVREARRHRV-LAVNGCLRPAINEEFTEREGRV 381
Db 260 WGVOKYRATITEICPMIIRTLVQPPSANDRQHLREVFMFLNLSQERKDFCERFGR 319
QY 382 QIGEFYGATECNCSIAN-----MDGKVGSCGNSRIL-PHYVPIRLVKNEDTME 430
Db 320 LLTS-YGMTEPIVIGIDRPGDKRWPISIGRAGFC-YDAEIRDDHNRPLPAGEIGE---- 373
QY 431 LLRDAOGLICPCQAGEPGLLVGINQODPLRRFDYGVYESATSKKTAHSVFGSGSAYLS 490
Db 374 -----ICI---KGVPGKTIK-----EYFLNPKATAKVL-----EADGWLHT 407
QY 491 GDVLVMDLGVMYFRDRSGDTFRWGENSVSTTEVEGLSRLLGQTDVAVYGVAVPGVEGK 550
Db 408 GDTGYRDEEGFFIFIDRRCNMRKGGNSVCELENIATHPKIQDILVVGVIK-DSIRDE 466
QY 551 AGMA-AVADPHSLLDPAIYQELQKVLAPYARPIELRLLPQVDTTGTGKTQKRLQ 605
Db 467 AIKAVVNLNGETLSEEEFFRCEQNNAKFKVPISYLEIRKDLPRNCSGKIIRNLK 522

RESULT 10

S40558

[illegible]

APGene: laud17
C:Superfamily: 4-coumarate--CoA ligase; acetate--CoA ligase homology
F:51-486/Domain: acetate--CoA ligase homology <ACL>

[illegible]

Db 415 TEVAVYVPVVDQVMAALVLAPGKTKFDADKFRALFTRQPDGLGHKQWPSYVVSAGLP 474

QY 593 TTGTFKIOKTRLOREGF---DP 611

Db 475 RTMTFKVKKRLSAGVACADP 496

RESULT 12

G70986

probable coA ligase - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis

C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 18-Aug-2000

C:Accession: G70986

R:Coile, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.

; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A:Reference number: A70500; MUID:98295987

A:Accession: G70986

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-532 <COL>

A:Cross-references: GB:295890; GB:AL123456; NID:g3242245; PIDN:CAB09316.1; PID:g2131015

A:Experimental source: strain H37RV

C:Genetics:

A:Gene: fadD1

C:Superfamily: 4-coumarate--CoA ligase; acetate--CoA ligase homology

F:48-499/Domain: acetate--CoA ligase homology <ACL>

Query Match 11.0%; Score 372; DB 2; Length 532;

Best Local Similarity 26.2%; Pred. No. 6.9e-22;

Matches 141; Conservative 82; Mismatches 221; Indels 94; Gaps 19;

QY 104 WTAQLDAYSNVANLFRQLGFGAPGVVAIFLEGRPEFVGLMLG-----LAKAGMBA 155

Db 27 WTSQYLAESAARA-----AALITADPQRTHIGSLGNTPEMLAQALAAAGLGG 76

QY 156 AL---LNVNLRREPLAFCLGTSGAKALIFGGMVAVAEVSGLHKLKFCSGDLGPG 212

Db 77 YVLCGLTTRGDALADVRRDCQIVTDDAHRALL-----DG 115

QY 213 I-LPDTHLDD---PLIKEASTAPLAQIPSGMD--DRLEFYIYTSGLTPKAAIVVHSRY 266

Db 116 LDLAGARILDTSPRAELVAGDGFVPYREVDMPPMMIIFTSGLSGNPKAVPVSH--- 172

QY 267 YRMAATGHHA---YRQADVLDCPLVHSAGNIIGVQCLLYGLTVLVRKKFSASRF 322

Db 173 -LMATFAGSLTERFGLTEQDTCYVSMPFLHSNNAVAGWAPVWSG-AAIAPATFSATGF 230

QY 323 WDCIKYNTCVQYIGEICRYLLKQPVREARRHVRVLAVGNLRPAIWEETFERFGRQ 382

Db 231 LDDVRYHATYMYVKPLAYILATPERDDADNPLURVAFGNEANDKJIEFSRRFGV-Q 289

QY 383 IGFYGATCNCNSIAMDG-KYVSCG-----FNSRILPHVPIRLVKVNDTWELLR 433

Db 290 VEDFGSTENAVIVIREPPTPGSIGRGAHVAVNGEIVTECAVARE----- 337

QY 434 DAQGLIPCQAGEPGLLVQINQDPLRFDFGVSE-SATSKIAHSVFSKSDSAYLSGD 492

Db 338 DAHAL--TNADE---AIGELVNTTGSFFTGYNDPEANERMRHGMVWSDLAY---- 388

QY 493 VLWMDLGYMYRDRSGDTFRWGENVSTTEGVLSRLLGQTDVAVYGVAVPGVEKAG 552

Db 389 ---RUSEGIYLAGTADMRVDGENLTAAPRIERILLRYKAINRVAVYAVPDEVYGDQVM 445

QY 553 MAADVPHSLDPNAI--YQELQKVLAPYARIFLRLLPQVDTTGTFKIOKTRLOREG 608

Db 446 AALVLRAGDTFDPDAFEAFDPAQPDLSKARPRYIRIADLPSTATHKVLKRLIDEG 503

RESULT 13

T03221

probable polyketide synthase module 1 - Streptomyces hygroscopicus

C:Species: Streptomyces hygroscopicus

C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 17-Nov-2000

C:Accession: T03221

R:Ruan, X.; Stassi, D.; Lax, S.; Katz, L.

Gene 203, 1-9, 1997

A:Title: A second type-I PKS gene cluster isolated from Streptomyces hygroscopicus

A:Reference number: Z14848; MUID:98085969

A:Accession: T03221

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-2723 <RUA>

A:Cross-references: EMBL:AF007101; NID:g2624946; PIDN:AAC38061.1; PID:g2624948

A:Experimental source: ATCC 29253

C:Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I homology; acetate--CoA

C:Keywords: carrier protein

F:54-504/Domain: acetate--CoA ligase homology <ACL>

F:881-949/Domain: acyl carrier protein homology <ACP1>

F:996-1397/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS>

F:1509-1794/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMT>

F:2568-2639/Domain: acyl carrier protein homology <ACP2>

Query Match 10.7%; Score 361; DB 2; Length 2723;

Best Local Similarity 27.5%; Pred. No. 5.3e-20;

Matches 156; Conservative 85; Mismatches 266; Indels 60; Gaps 20;

QY 64 VRLERRHQRAGHTIPRIFOAVVORPERLALVDAGTGCECTFAQLDAYSNVANLPROL 123

Db 2 LRRELIR-----PLPELLKAHARRGQSFADSRRCV--SYAQLERTRRLAGHLAQL 53

QY 124 GFAPQDVVAIFLEGRPEFVGLWGLAKAGMEALLNVNLRREPLAFCLGTSGAKALIFGG 183

Db 54 RLLPGDRAAIYLGNCVETIESYLATARASIGVPIPHSSPAELAYLLDLSAARVIVTDH 113

QY 184 EMWAABAVSVGHGKSLIKFCSGDLPBGILPDTHLLDPLKLEASTAPLAQIPSK---GM 240

Db 114 TRLQVRRLOAE-RPHLTVVVTG-D-EESGAVP----FDAL---AETEP---QOAPRDDGL 162

QY 241 DDRLFYIYTSGLTPKAAI-VVHSRYRYMAAFGHAYRMAQADVLDCLPLYSAGNII 299

Db 163 DDIAWMLYTSGLTPKGVLSQSLWSVAASSAGVLGLSETDRVLWPVPLFSLAHY 222

QY 300 GVGQCLYGLTVLVRKKFSASRFDDCKYKNTCTVVQYIGETCRYLLKQPVREAE---RRH 356

Db 223 CVLSVTAVGATARITEAFDAEELLTLRAEEFTFLAGVPTMYHYLL-DAARDGSLSPNL 281

QY 357 RVLAVGNGLRPAIWEETFERFGRQIGEEFYGATE-CNCSTANMDGKV---GSCGFNSRI 412

Db 282 RVLCSAGAISTATIRAEFOETFGVPL-LDCVGSSTETGLITANPNPQTQEGSCG----- 335

QY 413 LPHYPIRLVKVNEDTMELLRDAQGLCIPCQAGEPGLLVGINQDPLRRFDGTVVSESAT 472

Db 336 LP-VPLGTVRIVDPETHESVETGEEGI--WVGPSLMVGVHNPQPE-----ATEAAL 384

QY 473 SKKTAHSVFSKGD SAYLSGDVLMDELGYMTFRDRSGDTFRWGENVSTTEGVLSRL 532

Db 385 PR-----GWYRTGDLGRDDGLGYHTITGLSELIIIRSGENIHPTEVEQVLLRVP 433

QY 533 GQTDVAVGVAVPVEGKAGAAVADPSSLDPNAIYQELQKVLAPYARIFLRLLPQVD 592

Db 434 GVTDAAVVGSNPTL-GEVPVAVLVPADGDFDPDEFAACREHLAYFKVPEELYETGSIP 492

QY 593 TTGTFKIOKTRLOREGFDPQRTSDRLF 619

Db 493 RTGSGKIKRHALAQSAPRLRAVSSGSF 519

RESULT 14

E70853

probable acid--CoA ligase (EC 6.2.1.1-) fadD13 - Mycobacterium tuberculosis (strain

